

Figure 1

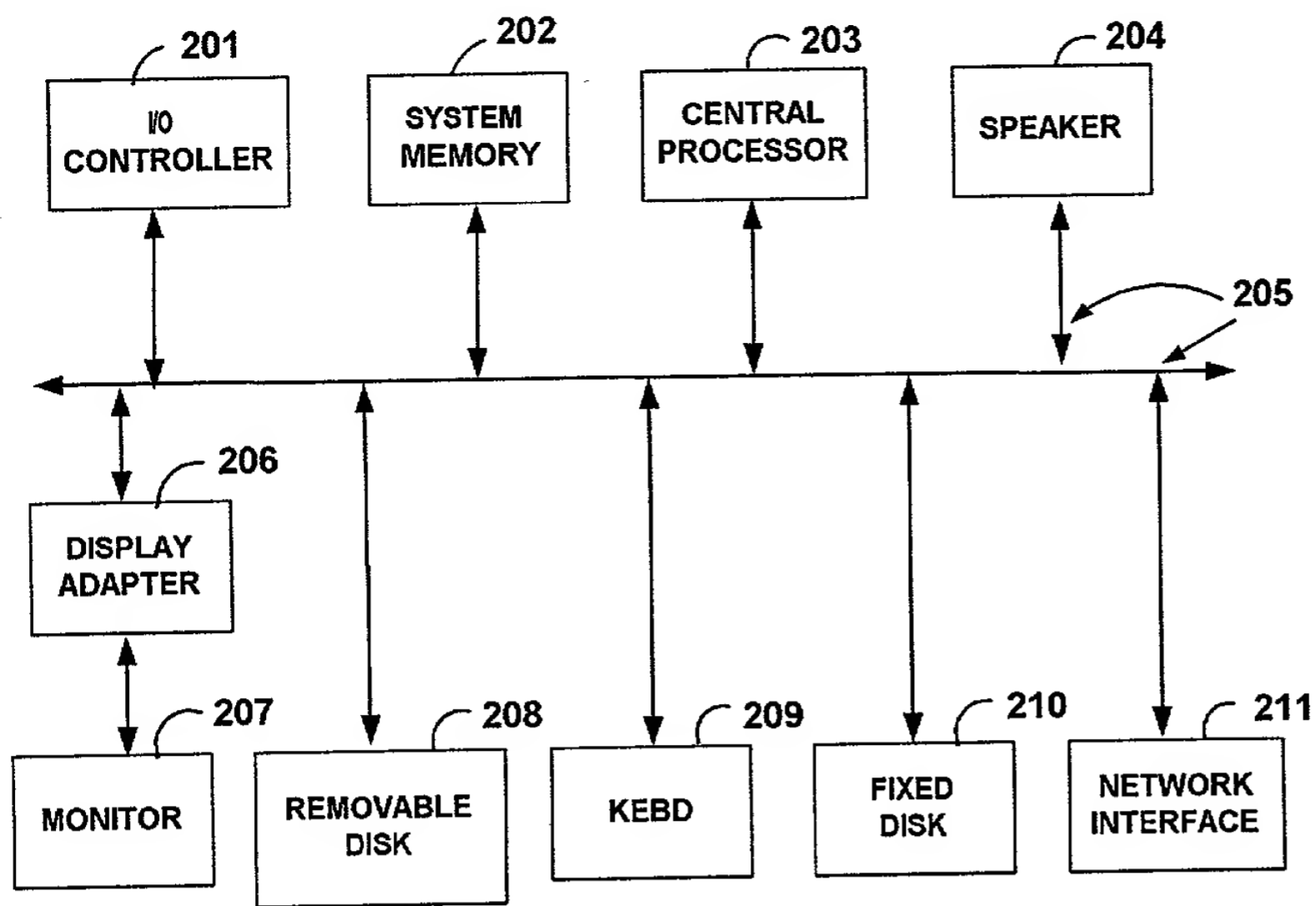


Figure 2

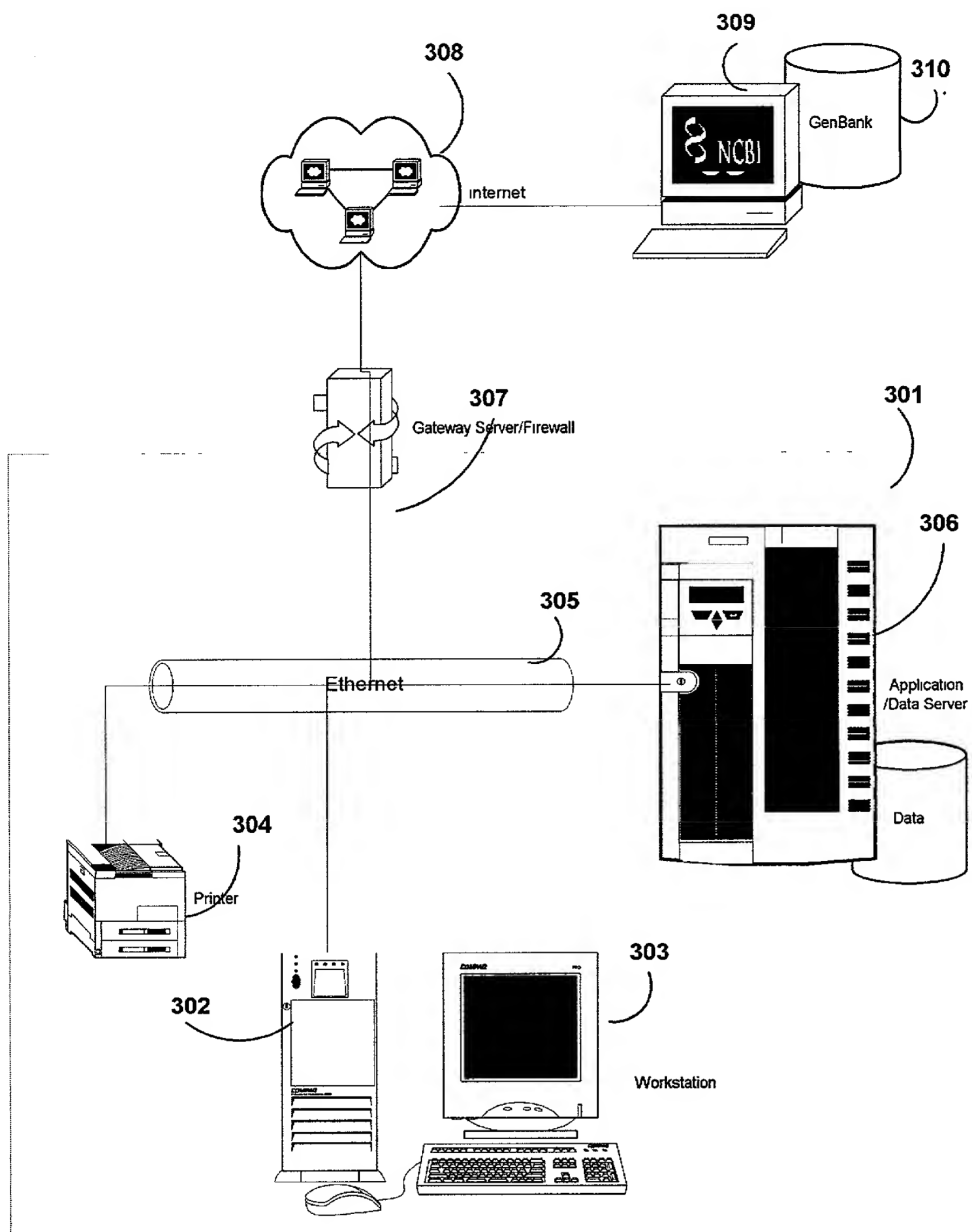
[illegible]

FIGURE 3

406027 498360

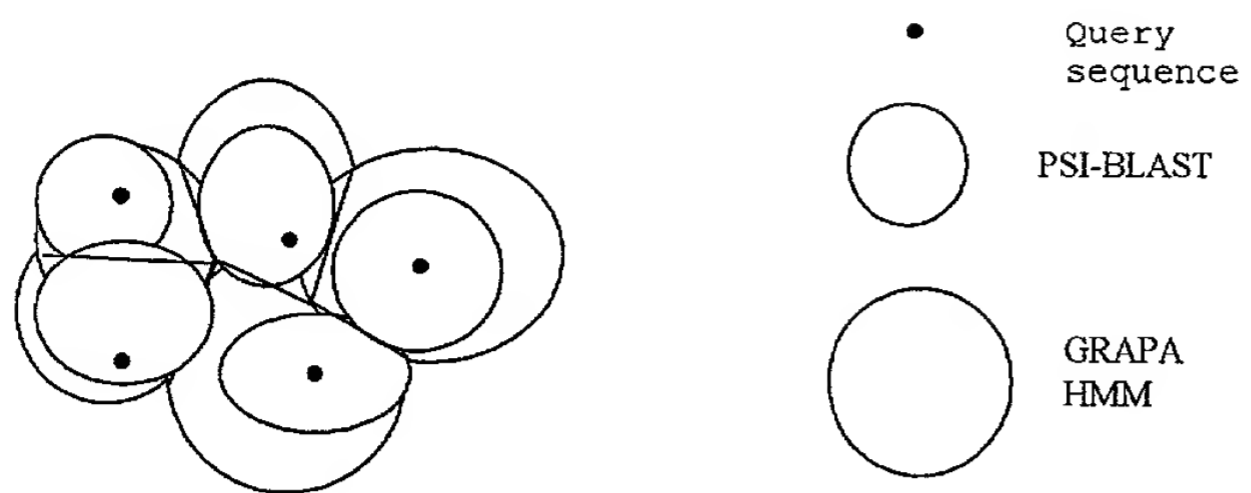


FIGURE 4

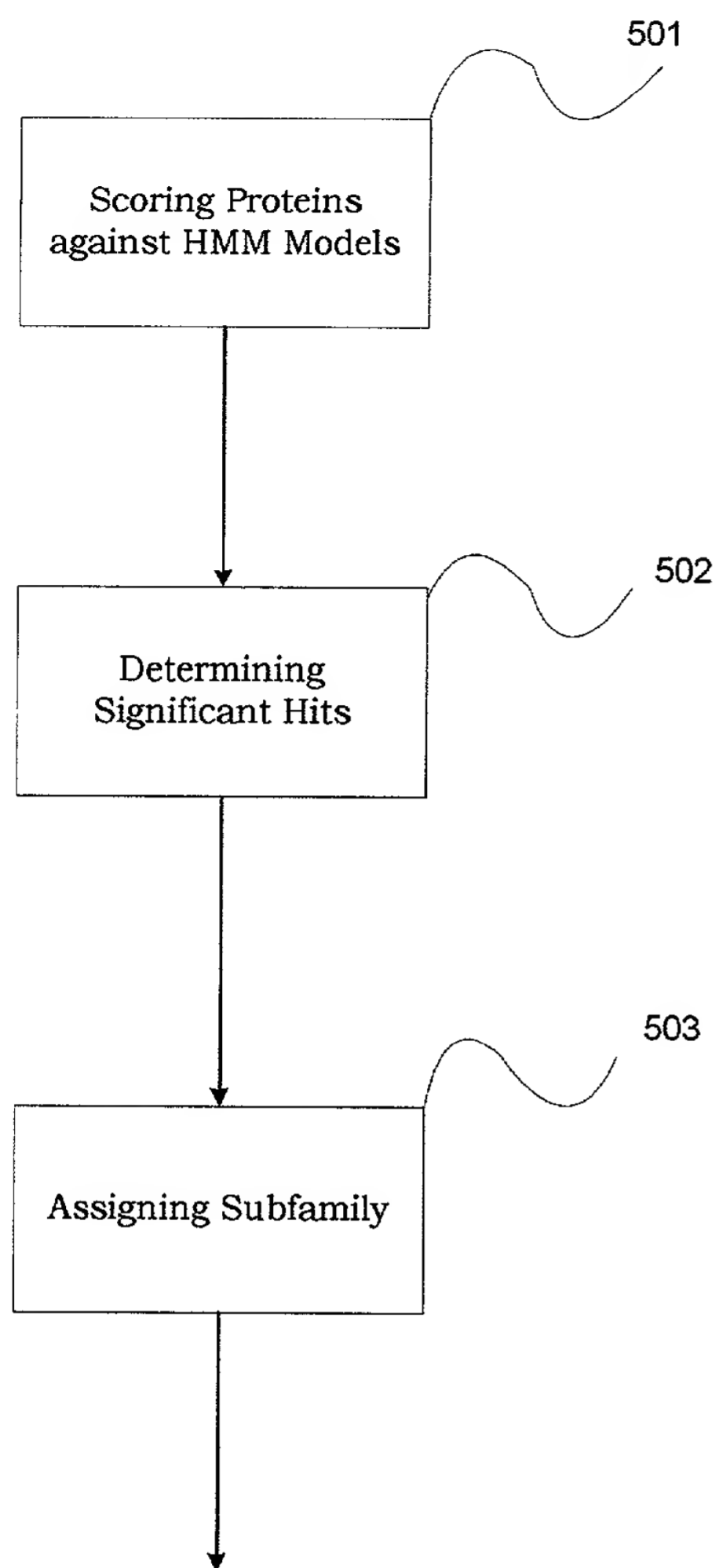


FIGURE 5

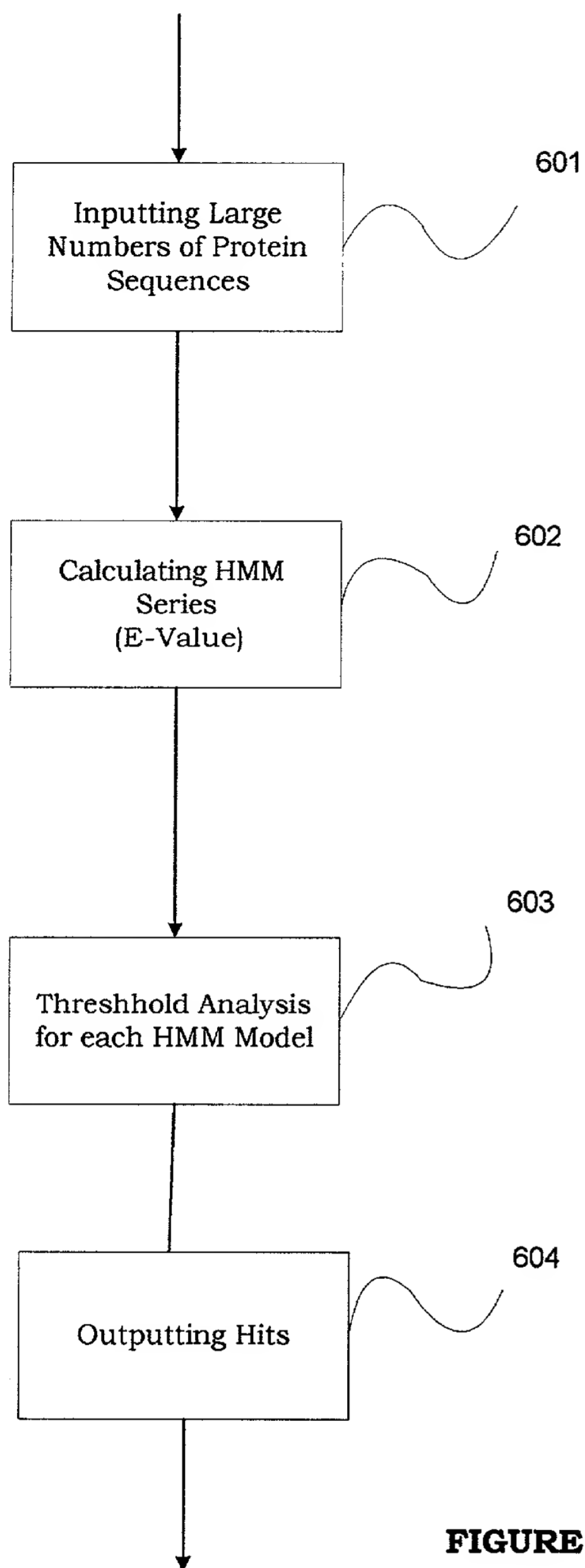


FIGURE 6

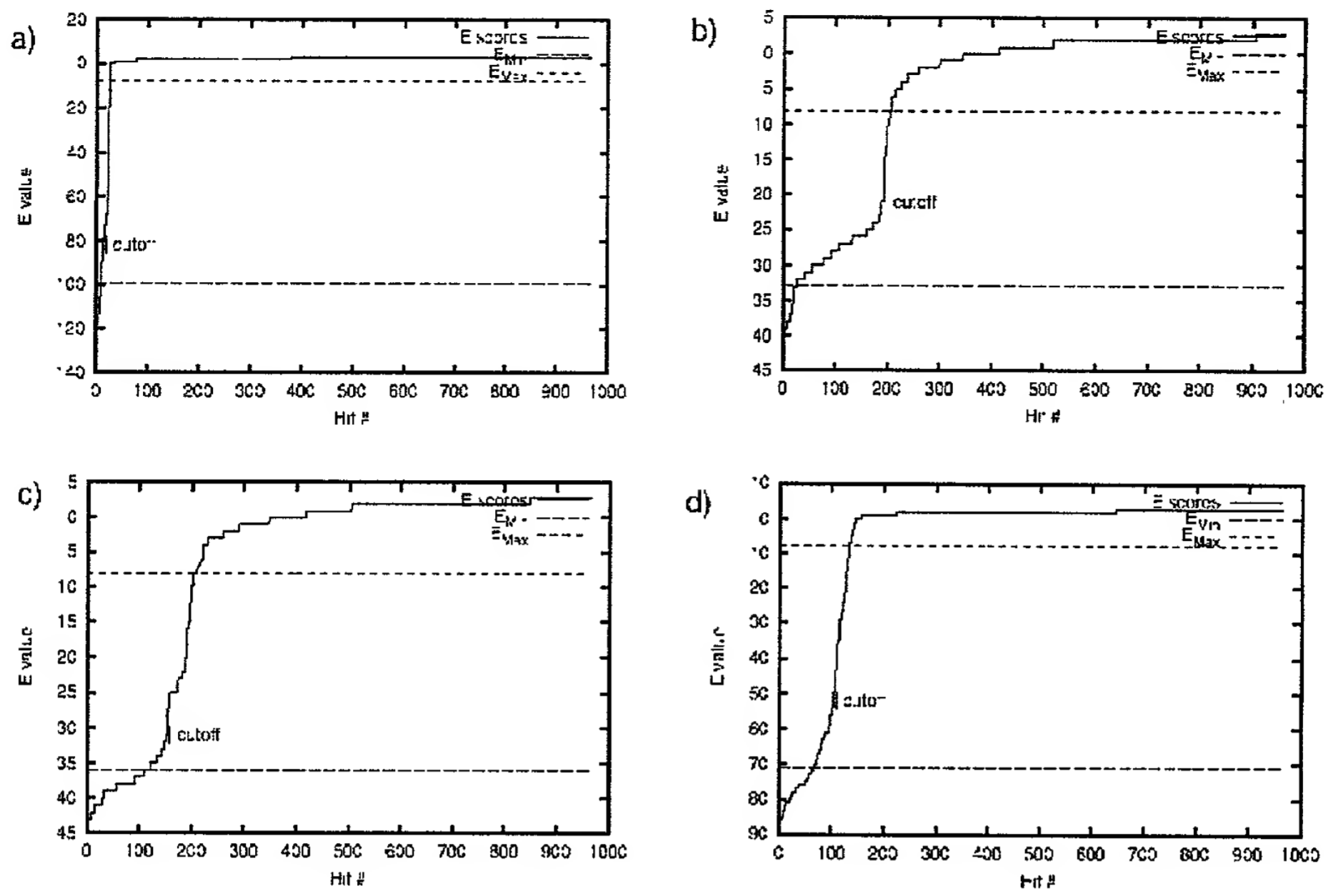


FIGURE 7

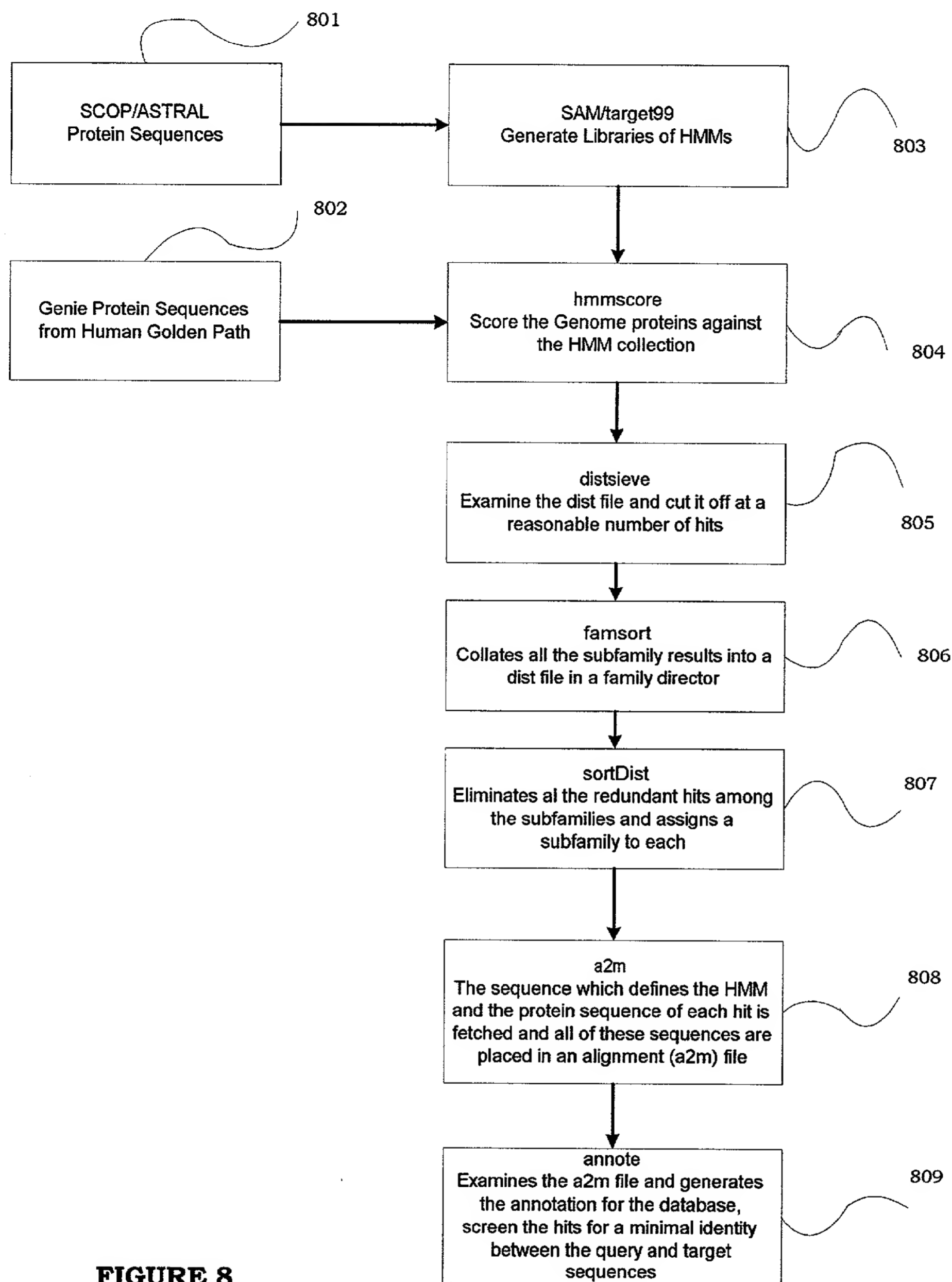


FIGURE 8

Alignment 1:

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1>GRAPAHIT1 1 LLQDSLLRLKDYRQCFCSDVALNEAVQQMVNSGEAAAKEEWVATVTQLL
2>lvhr 1 SVQDLNDLLSDGSGCYSLPSQPCNE VTPRIYVGNASVAQD IPKLQKL

1>GRAPAHIT1 51 MGIEQALSADSSGSILKVSSSTTGLVRLTNNLIQVIDCSMAVQEEAKEPH
2>lvhr 51 GITHVLNAAEGRSFMHVNTNAN

1>GRAPAHIT1 101 VSSVLPWIILHRIIWQEDTFHSLCHQQQLQNPAAEGMSETPMLPSSLML
2>lvhr 101 FYK DSGIT

1>GRAPAHIT1 151 LNTAHEYLGRRSWCCNSDGAALLRFYVRVLQKELAASTSEDTHPYKEELET
2>lvhr 151 YLGIKA NDTQEFN

1>GRAPAHIT1 201 ALEQCFYCLYSFSPKSKKARYLEEHSQQVDLIWEDALFMFEYFKPKTLP
2>lvhr 201 LSAYFERAA

1>GRAPAHIT1 251 EFDSYKTSTVSADLANLLKRIATIVPRTERPALSLDKVSAYIEGTSTVEP
2>lvhr 251 DF IDQALAQKNGRVL VH

1>GRAPAHIT1 301 CLPEGADPSPFPVVELLYLLADYHFKNKEQSKAIKFYMHDICICPNREDS
2>lvhr 301 C REGYSRSPTLV IAYLMR QKMDVKSALSIVRQNREIGPN DG

1>GRAPAHIT1 351 WAGMALARASRIQDKLNSNE LKS
2>lvhr 351 F LAQLCQLNDRLAKEGKLP

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Alignment 2:

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1a17 PPADGALKRAEELKTQAN-----DYFKAKDYENAIKFYSQAIE
GRAPAHIT2 PLCKQALEDLKTSQGHDPDVATMLNILALVYRDQNKYKEAAHLNDALA
GRAPAHIT3 KDWKGALDAFSAVQDPHSRICFN----IGCMYTILKNMTEAEKAFTRSIN

1a17 L-----NPSNAIYYGNRSLAYLRTECYGYALGDATR-AIELDKKYIK
GRAPAHIT2 IREKTLGKDHPAVAATLNNLAVLYGKRGKYKEAEPLCKR-ALEIREKVLG
GRAPAHIT3 R-----DKHLAVAYFQGMPLYQTEKYDLAIKDLKEALIQLRGNQLI

1a17 GYYRRAASNMA-----LG-----KFRAALRDYET-----
GRAPAHIT2 KFHPDVAKQLSNLALLCQNGKAEVEYYRRALEIYATRL----GPDDP
GRAPAHIT3 DYKILGLQFKLFACEVLYNIAFMYAKKEEWKAEQALALATSMKSEPRHS

1a17 -VVKVKP-----HDKDAKMKYQECNKIVKQKAF-----
GRAPAHIT2 NVAKTKNNLASCYLKQGYQDAETLYKEILTRAHEKEFGSVNGDNKPIWM
GRAPAHIT3 KIDKAMECVWKQKLYEPVVI PVGKLFPRNERQVAQLAKKDYLGKATVVAS

1a17 ---ERAIA-----GDEHKR-----SVVDSLDIESMTIEDEYS
GRAPAHIT2 HAEEREES-----KDKRRDSAPYGEYGSWKACKVDSPTVNTTLR
GRAPAHIT3 VVDQDSFSGFAPLQPQAAEPPPRPKTPEIFRALEGEAHRVLFGEV

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FIGURE 9

[illegible]